

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2001, 10:39:49 ; Search time 186.16 Seconds
(without alignments)
9305.869 Million cell updates/sec

Title: US-09-784-340-1

Perfect score: 2759
Sequence: 1 caaccatgcagatcagctgtc.....ctgtcagcgcgttaagcagc 2759

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

N_Geneseq_0601:*

1: /SIDSL/gcgcdata/geneseq/geneseqn/NA1980.DAT:*

2: /SIDSL/gcgcdata/geneseq/geneseqn/NA1981.DAT:*

3: /SIDSL/gcgcdata/geneseq/geneseqn/NA1982.DAT:*

4: /SIDSL/gcgcdata/geneseq/geneseqn/NA1983.DAT:*

5: /SIDSL/gcgcdata/geneseq/geneseqn/NA1984.DAT:*

6: /SIDSL/gcgcdata/geneseq/geneseqn/NA1985.DAT:*

7: /SIDSL/gcgcdata/geneseq/geneseqn/NA1986.DAT:*

8: /SIDSL/gcgcdata/geneseq/geneseqn/NA1987.DAT:*

9: /SIDSL/gcgcdata/geneseq/geneseqn/NA1988.DAT:*

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11: /SIDSL/gcgcdata/geneseq/geneseqn/NA1990.DAT:*

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16: /SIDSL/gcgcdata/geneseq/geneseqn/NA1995.DAT:*

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21: /SIDSL/gcgcdata/geneseq/geneseqn/NA2000.DAT:*

22: /SIDSL/gcgcdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	967.4	35.1	1650	21	AAZ65396	Human carboxylate
2	780.4	28.3	1976	21	AAZ95206	Human UDP-glucuron
3	775.6	28.1	2107	19	AAV15900	Uridine diphospho-
4	766	27.8	2092	21	AAZ95199	Human UDP-glucuron
5	750	27.2	1854	21	AAZ95200	Human UDP-glucuron
6	486.4	17.6	515	20	AAV87412	EST clone BR77. H
7	350	12.7	350	21	AAZ03286	Human secreted pro
8	317.8	11.5	2368	13	AAQ27370	HUG-Br2. Homo sap
9	316.6	11.5	2351	13	AAQ27369	HUG-Br1. Homo sap
10	272.2	9.9	735	21	AAZ45118	UDP-glucuronosyltr
11	200.2	7.3	2312	21	AAZ95207	Human UGT2B15 exon

12	196.4	7.1	936	22	AAZ95252	Oligonucleotide D1
13	196.4	7.1	936	22	AAZ95254	Oligonucleotide D1
14	196.4	7.1	936	22	AAZ95257	Oligonucleotide D1
15	196.4	7.1	936	22	AAZ95259	Oligonucleotide D2
16	196.4	7.1	936	22	AAZ95262	Oligonucleotide D2
17	196.4	7.1	938	22	AAZ95255	Oligonucleotide D1
18	195.8	7.1	1323	21	AAZ95193	Human UGT2B4 exon
19	195.4	7.1	936	21	AAZ95205	Human UGT2B7 exon
20	194.2	7.0	936	22	AAZ95252	Oligonucleotide D1
21	194.2	7.0	936	22	AAZ95254	Oligonucleotide D1
22	194.2	7.0	936	22	AAZ95257	Oligonucleotide D1
23	194.2	7.0	936	22	AAZ95259	Oligonucleotide D2
24	194.2	7.0	936	22	AAZ95262	Oligonucleotide D2
25	194.2	7.0	938	22	AAZ95255	Oligonucleotide D1
26	193.8	7.0	938	22	AAZ95257	Oligonucleotide D1
27	188.4	6.8	978	21	AAZ95211	Human UGT2B4 exon
28	179.8	6.5	1686	21	AAZ95198	Human UGT2B7 exon
29	145.6	5.3	391	20	AAZ95201	Human lung tumour
30	145.6	5.3	391	21	AAZ95208	Human lung tumour
31	144.8	5.2	1602	21	AAZ95210	Human UGT2B15 exon
32	144.6	5.2	1591	21	AAZ95204	Human UGT2B7 exon
33	143.2	5.2	2320	21	AAZ958107	Human PRO1780 (UNG)
34	143.2	5.2	2320	21	AAZ958107	Human PRO1780 (UNG)
35	143.2	5.2	2320	22	AAZ954401	Primer #82 used in
36	141.6	5.1	2341	22	AAZ93775	Human cDNA encodin
37	138.6	5.0	689	21	AAZ95197	Human UGT2B4 exon
38	132.8	4.8	283	21	AAZ87467	Rat hepatocyte car
39	131	4.7	223	21	AAZ87255	Rat hepatocyte car
40	120.2	4.4	1020	21	AAZ95208	Human UGT2B15 exon
41	114	4.1	164	21	AAZ87154	Rat hepatocyte car
42	110.2	4.0	273	21	AAZ87491	Rat hepatocyte car
43	109.8	4.0	746	21	AAZ95194	Human UGT2B4 exon
44	101.4	3.7	1340	21	AAZ95202	Human UGT2B7 exon
45	98.6	3.6	1822	21	AAZ95203	Human UGT2B7 exon

ALIGNMENTS

RESULT	1
AAZ95396	AAZ95396 standard; cDNA; 1650 BP.
ID	XX
XX	AAZ95396;
AC	XX
XX	13-FEB-2001 (first entry)
DT	XX
XX	XX
DE	Human carboxylate-modifying enzyme cDNA Incyte ID No: 2912330CB1.
XX	XX
KW	Human; carboxylate-modifying enzyme; CME; antidiabetic;
KW	immunosuppressive; anti-HIV; antiinflammatory; antinaemic;
KW	antisthmatic; antiarteriosclerotic; antihypoid; hepatotropic;
KW	nephrotropic; antiout; thymimetic; neuroprotective; osteopathic;
KW	antiarthritic; antiproliferative; uropathic; ophthalmological;
KW	dermatological; antitumor; cytostatic; vituicide; antibacterial;
KW	fungicide; protozoicide; tranquilliser; vulnary; diabetes;
KW	autoimmune disorder; inflammatory disorder; infection; ss.
XX	XX
OS	Homo sapiens.
XX	XX
PN	W0200063351-A2.
XX	XX
PD	26-OCT-2000.
XX	XX
PF	20-APR-2000; 2000MO-US10882.
XX	XX
PR	21-APR-1999; 99US-0130383.
XX	XX
PA	(INCY-) INCYTE GENOMICS INC.
XX	XX
PI	Lal P, Yue H, Tang YT, Hillman JL, Baughn MR, Yang J;
XX	XX
DR	WPI; 2000-672729/65.

Done UDP glucuronosyl transferases

DR P-RSD: AAB28677.
 XX
 PT Novel carbohydrate modifying enzyme polypeptides and polynucleotides
 PT for diagnosis, treatment and prevention of carbohydrate metabolism
 PT disorders, autoimmune/inflammatory disorders, and cancer
 XX
 PS Claim 4; Page 75; 75pp; English.
 XX
 CC The present cDNA sequence encodes a human carbohydrate-modifying enzyme
 CC (CME). CME polynucleotides and polypeptides are useful for treating and
 CC diagnosing diseases associated with CME such as diabetes,
 CC autoimmune/inflammatory disorders such as AIDS, Addison's disease,
 CC adult respiratory distress syndrome, allergies, anaemia, asthma,
 CC atherosclerosis, autoimmune thyroiditis, bronchitis, cholecystitis,
 CC contact dermatitis, Crohn's disease, emphysema, erythroblastosis fetalis,
 CC glomerulonephritis, Good pasture's syndrome, gout, Grave's disease,
 CC Hashimoto's thyroiditis, multiple sclerosis, myasthenia gravis,
 CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
 CC Reiter's syndrome, arthritis, scleroderma, Sjogren's syndrome, systemic
 CC lupus erythematosus, ulcerative colitis, uveitis, Werner syndrome,
 CC complications of cancer, haemodialysis, and extracorporeal circulation,
 CC viral, bacterial, fungal parasitic, protozoal, and helminthic infections,
 CC trauma, or cancer. CME, or its catalytic or immunogenic fragment, is
 CC useful for drug screening.
 CC
 XX
 SO Sequence 1650 BP; 489 A; 330 C; 354 G; 477 T; 0 other;

Query Match 35.1%; Score 967.4; DB 21; Length 1650;
 Best Local Similarity 75.7%; Pred. No. 3, 3e-187;
 Matches 1228; Conservative 0; Mismatches 386; Indels 9; Gaps 2;

QY 34 catcatagagctgcacagcagcttgatcttgctcctcagctcctgt---gt 90
 DB 28 catcagagatgctatgaagatgcagctcctcctcctcctgatacagctgagctgtaactt 87
 QY 91 tggctgagcttcctgaggaagctcctgctgctgctgctgagcagctgagcagctgagcctaa 150
 DB 88 tactctgagagctgaggaagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 147
 QY 151 tgcacagctcatctagaagctcagctagtgagagcagcagcagcagcagcagcagcagcagc 210
 DB 148 tataagacacatcctgataactgtccagagagctcagagctgagctgagctgagctgagctc 207
 QY 211 ctcaagagctcgttaattgactacaggaagcctctgctcagctgaattgagctgagctgagc 270
 DB 208 ttcagcttcattcttcctgatacctcagcagcagcagcagcagcagcagcagcagcagcagc 267
 QY 271 tatgcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 324
 DB 268 tgcattcttaactaaacagcagcttgagagatataccaagcagcagcagcagcagcagcagc 327
 QY 325 tgcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 384
 DB 328 agaacctccaagaagacacatttgctacatatttccacaagagtaagaacatcatgagac 387
 QY 385 aataagaggaactttaaaatgatgtgtagagccttatctacaacacagaagcctttagaa 444
 DB 388 atttaatgacatactagaagaagctcgttaagaatatttccaataaagaacatcatgaa 447
 QY 445 gaagctacaggaac 504
 DB 448 gaacactacagagctcaagcttgatgttcttgtagagctgctgcttcccttcttgtaga 507
 QY 505 cctgctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctg 564
 DB 508 gctgctgagcagcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 567
 QY 565 caataatgagcagagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 624
 DB 568 cgcatttgaagaagcagtagtgagagcagcttctgctcctcctcctcctcctcctcctcctc 627
 QY 625 gacagagactaacagacagatgaccttctcgtgaagaagtaaaaattcaatgcttccagct 684

DB 628 gtccgaactaagtgaccaaagacttcaatagagagggtaaaaatagactatgct 687
 QY 685 ttgttccacttcctgagctcagcagcttaacagactaattttggggaagctttatagaa 744
 DB 688 ttatttgaatttggttccaaatatttgatagaagaagtgagatcagcttccatgta 747
 QY 745 ggcattgggaagccccaactacatattatgtgagctgctggaaagcctgagatagctat 804
 DB 748 agtcttagaagaccactacagctatctgagacatgagcaaaagcagacatagcttat 807
 QY 805 acgaacattggagatttgatcttccaaacccatcacacactacactttagttgttg 864
 DB 808 tcgaactacagtgagatttcaatcttccacacaccccttaccacaaatgctttagcttg 867
 QY 865 agatgacatgtaaacctgcacaaagcttgcctaaagaaatgtaaaatctgtgcagag 924
 DB 868 agagctcactgcacaaacctgcacaaacccctaccgaagaaatggaagtgtgtccagag 927
 QY 925 ttcaggggaagatgcttctgtgtgttcttctgtggttgcacatgttcaaaatgtacaga 984
 DB 928 cctctgagaaatggtgtgtgtgtgttcttctgtggtgtgagtgagtaacagctcaga 987
 QY 985 agaaaagcctaatactctcagccttgcagcctgcccagatcccaagaggtgtatagag 1044
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 QY 1045 gtacaaaggaaaaaaacacacacacataggaagcacaactcgtgctatagattgatacc 1104
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 QY 1105 ccgaatgactctctgtgctacatcccaaaacaaagctttatatactatggttgatgaa 1164
 DB 1108 ccgaatgactctctgtgctacatcccaaaacaaagctttatatactatggttgatgaa 1167
 QY 1165 tgggactatgaagcattattacatgagctggtccctatggtgagcttccacatgtgtga 1224
 DB 1168 tgggactatgaagcattattacatgagctggtccctatggtgagcttccacatgtgtga 1227
 QY 1225 tcaagctgataacatgctcagatgaagcagcagcagcagcagcagcagcagcagcagcagc 1284
 DB 1228 tcaagctgataacatgctcagatgaagcagcagcagcagcagcagcagcagcagcagcagc 1287
 QY 1285 aactatgacaaagcagatcttactgagcgttgaagaacagatcatcagatccctcta 1344
 DB 1288 aactatgacaaagcagatcttactgagcgttgaagaacagatcatcagatccctcta 1347
 QY 1345 taaaggaatgctatgagattatcaagaattcaacatgacacactgttaaagccctaga 1404
 DB 1348 taaaggaatgctatgagattatcaagaattcaacatgacacactgttaaagccctaga 1407
 QY 1405 tcgaagcagctcttgatgagcttctgcatgcccagaagagcagcagcagcagcagcagcagc 1464
 DB 1408 tcgaagcagctcttgatgagcttctgcatgcccagaagagcagcagcagcagcagcagcagc 1467
 QY 1465 agctgccatgac 1524
 DB 1468 agctgccatgac 1527
 QY 1525 gacccgtgtggcagcagctatcttctgttcaaaaatgtttttatttcttctgtcca 1584
 DB 1528 gacccgtgtggcagcagctatcttctgttcaaaaatgtttttatttcttctgtcca 1587
 QY 1585 atttaataaactagaaagatagaagaagggagatagatcttccaatccaagaagag 1644
 DB 1588 atttaataaactagaaagatagaagaagggagatagatcttccaatccaagaagag 1647
 QY 1645 ctg 1647
 DB 1648 ctg 1650

RESULT 2


```
QY 1283 aaactatgacgaagcgaattacttgaaggctttgaagacagctcatcaccattcctc 1342
DB 1265 aggcacatgcaagtgatgagattgttcccaatgcatltaagtcacgcatlaatgacccgtgc 1324
QY 1343 tataaagagaatctatagatatacaagaatcacatgatacctgtaagccctca 1402
DB 1325 tataaagagaatctatagatatacaagaatcacatgatacctgtaagccctc 1384
QY 1403 gacgagcagctcttctgagctgagttgtatgcgcacaaagagcgaagcagcctgcga 1462
DB 1385 gacgagcagctcttctgagctgagttgtatgcgcacaaagagcgaagcagcctgcga 1444
QY 1463 tcagctgcccattacacactcagctgttcacagcactcctatagtatgtatgttgcctc 1522
DB 1445 gtcgacagctacacactcagctgttcacagcactcctatagtatgtatgtatgtatgcctc 1504
QY 1523 ctgacactgtgtgagcagctgctatattctgttcaacaaatgttttatttctcgtca 1582
DB 1505 ctgagctgtgtgagcagctgctatattctgttcaacaaatgttttatttctcgtca 1564
QY 1583 aaattcaataaactagaagaagatagaaggaatagatcttcccaattcaagaag 1642
DB 1565 aagctgtgcaaaaacaggaagaagaagaagaagatgataatcaaaagcctgaagt 1624
QY 1643 acctga 1648
DB 1625 gaatga 1630

RESULT 3
AAV15900
ID AAV15900 standard; cDNA; 2107 BP.
AC AAV15900;
XX
XX 26-MAY-1998 (first entry)
XX
XX Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.
XX Uridine diphospho-glucuronosyltransferase 2B17; UGT2B17; catalyze;
XX androstereone; androstereone-glucuronic acid; androgen; enzyme; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX 5'UTR 1..51
XX CDS /*tag= a
XX /*tag= 52..1644
XX /*tag= b
XX /*product= "UGT2B17 enzyme"
XX 3'UTR 1645..2107
XX /*tag= c
XX
XX WO9744466-A1.
XX
XX 27-NOV-1997.
XX
XX 16-MAY-1997; 97WO-CA00328.
XX
XX 17-MAY-1996; 96US-0649319.
XX
XX (ENDO-) ENDORCHERCHE INC.
XX
XX Beaulieu M, Belanger A, Hum DW, Levesque E;
XX
XX WPI; 1998-018520/02.
XX
XX P-PSDB; AAM47126.
XX
XX DNA encoding uridine di-phospho-glucuronosyl-transferase 2B17 -
XX which catalyses conversion of androstereone to
XX androstereone-glucuronic acid
XX
```

```
PS Claim 15; Pages 4-6; 53pp; English.
XX
XX This cDNA encodes an enzyme uridine di-phosphoglucuronosyltransferase
CC 2B17 (UGT2B17). This novel enzyme catalyzes the conversion of
CC androstereone to androstereone-glucuronic acid. The UGT2B17 can be used to
CC detect anti-UGT2B17 antibodies. The antibody can be used to detect a
CC localized concentration of UGT2B17 or an alteration in androgen activity.
CC The UGT2B17 can also be used to alter the concentration of an androgenic
CC compound in a tissue, specifically dihydrotestosterone. An isolated
CC nucleotide sequence comprising at least 30 consecutive nucleotides from
CC the coding region of the 2107 base pair sequence, or its complement can
CC be used to block the synthesis of UGT2B17, e.g. an expression disrupting
CC sense or antisense fragment, or as a probe for a UGT2B17 coding sequence.
XX
XX Sequence 2107 BP; 657 A; 382 C; 424 G; 644 T; 0 other;
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Query Match 28.1%; Score 775.6; DB 19; Length 2107;
Best Local Similarity 68.3%; Pred. No. 2,6e-148;
Matches 1110; Conservative 0; Mismatches 504; Indels 12; Gaps 2;

QY 35 atcatgagctctgacagctcagcttggatcttctgtctcctcagctctctcgt---gtt 91
DB 46 accagagatgtctctgaaatgagatgctcagctcttctgtatgacagctcagcttctt 105
QY 92 ggcctgtgagctctgtggaagctccctgctgtgagcctgtgacatgagcctgcttaat 151
DB 106 agctctgagagtggtggaagtgctgtggtggtggtggtggtggtggtggtggtggtggt 165
QY 152 gtcaaggtcattctagaagagctcagatgtagagagcagatgagtaacagatgagtcac 211
DB 166 atgaagacacatcctggaagagctgtgacagagggatgagtgatgtgtgtgtgacatc 225
QY 212 tcaagcctctgtaattgactacaggaagccttctgcttgaattgaattgagtggtccat 271
DB 226 tggctctcattctgtgcaatgacgaataatcctgcatatgaattagaattatcct 285
QY 272 atgccaagagacagaacaagaagaatgaataatc-----gttacctagctcgt 322
DB 286 acatccttaacaaatgatttggaagcttcttcttgaatgtaagatgtaagatgagaa 345
QY 323 aatgtcttccagcgttatacaactgtgcaatcagttataaataatgaattcttctgt 382
DB 346 tatagatattcaaaaatacatttggatatttttcaacaactaagaattgtgtgtg 405
QY 383 gaataaagaggaacttaaaatgagtgtgtgagagcttatacacaatgaagcgttctg 442
DB 406 gaatattctgactataataaagctcgtggaagatgcagtttgaacaagaacttatg 465
QY 443 aagaagctacaggaacaacaactacgagtgaatgataagcctgtgattcctgtgga 502
DB 466 agaaactacagaagtcaaaatttgatgtccttcgtgagatgcgctgaatccctgtgt 525
QY 503 gacctgagctgagtggtgtgtgcaatccttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 562
DB 526 gagctgtgagcgaactacataacacacacacacacacacacacacacacacacacacac 585
QY 563 ggcacatgagcagagctgtgtggaacttccagctcagcttccctcagatgactgtgct 622
DB 586 tacacagttgagaagaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 645
QY 623 atgacagactaacagacagaatgaccttctggaagaagtaaaaatcaatgacttca 682
DB 646 atgcaagaatttaagtaaatgatttctcagtgagagataaaaatatatataatg 705
QY 683 gttgtgcacacttctgagctcagatgagactatccttcttggagagagtttatgt 742
DB 706 cttaatttgaacttgtgttcaagcatalgactggaaggtgtggacacagtttatgt 765
QY 743 aagcattaggaagccacacacacacacacacacacacacacacacacacacacacacac 802
DB 766 gaagttctaggaagccacacacacacacacacacacacacacacacacacacacacacac 825
```

```
QY 803 atacaacatacttgatgttgaattctcctcaacataccaacttaatttgatt 862
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 826 atcgaacacttcttgatgttgaattctcctcgcacattctcaacaatgttatt 885
QY 863 ggaagatgacgtttaaactgcacaaagcttgccttaagaaatgaaatattgtcc 922
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 886 ggaagacttctacttaaccgcaaacaccttgcttaagaaatgaaagattgtgcag 945
QY 923 agttcagaagggaagtgtgtattgtgttcttctctggtggtcactggttcaaatgttaca 982
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 946 agcctcgaagaatggtatgtgtgttctctcgtggtggtcgtatcgaatgaatgca 1005
QY 983 gaagaagaagctaatatcattgcttcagcccttgccagatcccaagaagtgattag 1042
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1006 gaagaagaagctcaacatgattgcttcagcccttgccagatcccaagaagtgattag 1065
QY 1043 aggtacaagaagaaaaaacctccacattagaagcaatactgcgctgattgata 1102
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Db 1066 agatttgatgcagaagaagcaaatattcttagttccaataactgactgattatagtgta 1125
QY 1103 ccccaagaatgactcttctgtgtcattcccaaaacaaagcttatacactatggtgaaatg 1162
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1126 ccccaagaatgactcttctgtgtcattcccaaaacaaagcttatacactatggtgaaac 1185
QY 1163 aatggatctatgaagctattaccatggtggtccctatggtggaagttcccatattggt 1222
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1186 aatggatctatgagcgtatgacatccatggtggtccctatggtggaagttcccatattggt 1245
QY 1223 gataagttataacatagctacatgaagcaagaagagcagctgtgaataatactt 1282
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1246 gatcaaatgataacatgacatgacatgaagaagcaagagcagccctcaggtgtaacatc 1305
QY 1283 aaaaactatgacaagaagatacttctgagggcttgaagaacagtcacatccgattcctct 1342
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1306 aggaacatgtcaagtagaatttctcattgacatgaagtcacatgaagtcacatgaagtcac 1365
QY 1343 tataaagaagaatgtatgagatatacaagaattcaacatgatacctgttaaacctcta 1402
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1366 tataaagaagaatatacaagaattatacaagaattcaacatgatacctgttaaacctcta 1425
QY 1403 gatacgaagctctctgtatgagattgttcacatgcgcaagaagagcagcactgtgca 1462
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1426 gatcgaagcagctctctgtatgagattgttcacatgcgcaagaagagcagcactgtgca 1485
QY 1463 tcagctgcacatgacactcaccctggttccagcactactatagatgtgattggttccctg 1522
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1486 gtccgacagcccaacacactcaccctggtatccagcactacttggatgtgattgacatccctg 1545
QY 1523 ctgacccgtgtggaactgtcatattcttcttcaacaagaatgttttatttctctgtcaca 1582
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1546 ctgacccgtgtggaactgtcatattcttcttcaacaagaatgttttatttctctgtcaca 1605
QY 1583 aaattataaataacatagaagaagaggaatagatcttcccaattccaagaaga 1642
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1606 aagcttgcacaaagaagaagaagaagaagaagattcagttatatacaaaacccgtgaagt 1665
QY 1643 acctga 1648
  |||
Db 1666 gaatga 1671
```

RESULT 4

AAZ5199 ID AAZ95199 standard; DNA; 2092 BP.

XX AC AAZ95199;

XX DT 05-JUN-2000 (first entry)

XX DE Human UDP-glucuronosyltransferase 2B4 nucleotide sequence.

XX KM UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;

KW drug interaction; detect; human; single nucleotide polymorphism; ds.

```
XX OS Homo sapiens.
XX PN WO200006776-A1.
XX PD 10-FEB-2000.
XX PF 22-JUL-1999; 99WO-US16675.
XX PR 28-JUL-1998; 98US-0094391.
XX PA (AXYS-) AXYS PHARM INC.
XX PI Galvin M, Miller A, Penny L, Riedy M.
XX DR WPI; 2000-195321/17.
XX DR P-PSDB; AAY78933.
XX PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
XX PS genotyping individuals to predict rate of metabolism of substrates and
XX PS for identifying potential drug interactions
XX PS Disclosure; Page 34-36; 72pp; English.
```

This sequence represents the human UDP-glucuronosyltransferase 2B4 (UGT2B4) gene. UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyze the glucuronic acid conjugation of a wide range of endogenous and exogenous substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms in the liver. Alteration of the expression or function of UGTs may effect drug metabolism. The invention relates to non-chromosomal nucleic acid molecules, which comprise human UGT2B sequence polymorphisms (see AAZ95051-295110). Probes which detect the UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism of a substrate in an individual. The nucleic acid molecules comprising a human UGT2B sequence polymorphism can be used in screening assays for genotyping individuals, also to predict their rate of metabolism of UGT2B substrate, potential drug-drug interactions and adverse side effects. The polymorphisms can be used as single nucleotide polymorphisms (SNPs) for detecting genetic linkage related to phenotypic variation in activity or expression of UGT2B protein. The polymorphism containing CC nucleic acid molecules may also be used for generating genetically modified non-human animals and for obtaining site specific gene modification in cell lines.

XX SQ Sequence 2092 BP; 639 A; 398 C; 438 G; 617 T; 0 other;

Query Match 27.8%; Score 766; DB 21; Length 2092;

Best Local Similarity 68.7%; Pred. No. 2.3e-146; Matches 1102; Conservative 0; Mismatches 490; Indels 12; Gaps 3;

```
QY 34 catcatgagctgtacaaagctgtgtattctgtcctcctgacgtcttctgt 90
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 catcagagatgtcatgaagaatgactcagctctctgtcgtatagctgagctgttact 90
QY 91 tgcctgtgattctgtgtggaagctcgtgtgtggtccctgtgacatgtgacctgtgctaa 150
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 tagctctggagtggtgtggaagctcgtgtgtggtcccaagaattcagcactgtgagaa 150
QY 151 tgcataagctatctagaagaagctcagtagagagagcagataggttaacagtagtactca 210
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 tataaagaacaactcgtatgtaactgttccagagagagcagagagtgatgtatggacatc 210
QY 211 ctcaaaagccttcgttaattgactacagaagacctctgcattgaaattgagtggtcaca 270
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 ttacgcttcaattcttcttgatcccaacagcccatctactcttaattgaaatttacc 270
QY 271 tatgcacaagagacagcaagaagaatgaaatttctgtgacttaactcga-----a 324
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 271 tgtatcttaactaaactagtttgagatatataaagcagctgtgttaagagatgggc 330
QY 325 tgccttgcagagctatcaacacctgcaatcagttataaattatattttttgtga 384
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries
 PS Claim 1; Page 556; 633pp; English.

CC This sequence represents an expressed sequence tag (EST), and is a
 CC polynucleotide of the invention. The polynucleotides of the invention are
 CC all secreted EST sequences isolated from a variety of human tissue
 CC sources. The EST sequences and proteins encoded by them are predicted to
 CC have useful biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC therapy. The EST sequences are also stated to be useful for gene

XX Sequence 515 BP; 148 A; 98 C; 122 G; 147 T; 0 other;

Query Match 17.6%; Score 486.4; DB 20; Length 515;
 Best Local Similarity 99.8%; Pred. No. 8e-90;
 Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 gaatgcacatcatgaagctctacacagctggtgattcttctcctgagctcttct 86
 DB 22 gaactgcacatcatgaagctctacacagctggtgattcttctcctgagctcttct 81
 QY 87 gctgtgctgtgagctctctggtggaagctcctggtggtcctgagcatgagcattg 146
 DB 82 gctgtgctgtgagctctctggtggaagctcctggtggtcctgagcatgagcattg 141
 QY 147 ttaatgcacagctcatctcgaagctcgaagctcgaagctcgaagctcgaagctcga 206
 DB 142 ttaatgcacagctcatctcgaagctcgaagctcgaagctcgaagctcgaagctcga 201
 QY 207 ctaactcaagcctctgtaattgactacaggaagcctctgactcaatgaattgaggtg 266
 DB 202 ctaactcaagcctctgtaattgactacaggaagcctctgactcaatgaattgaggtg 261
 QY 267 tcaatgcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 326
 DB 262 tcaatgcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 321
 QY 327 tcttgcacagcctatcaacctggaatcaatttaataaattgattttttgttgaa 386
 DB 322 tcttgcacagcctatcaacctggaatcaatttaataaattgattttttgttgaa 381
 QY 387 taagaggaacttaaaatgagtgtgagagcttactctacacagcagcattgaaga 446
 DB 382 taagaggaacttaaaatgagtgtgagagcttactctacacagcagcattgaaga 441
 QY 447 agctacaggaacacactcagatgattgattatagaacctgagattcctgtggagacc 506
 DB 442 agctacaggaacacactcagatgattgattatagaacctgagattcctgtggagacc 501
 QY 507 tgatgagct 514
 DB 502 tgatgagct 509

RESULT 7

AC03286 AAC03286 standard; cDNA; 350 BP.

AC03286; AAC03286;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 3284.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 OS Homo sapiens.

XX EPI033401-A2.
 XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

XX P-PSDB: AAG03280.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PS Claim 1; SEQ ID 3284; 71pp + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC well suited for isolating cDNA libraries. Such ESTs are not
 CC often obtained for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.

XX Sequence 350 BP; 108 A; 69 C; 77 G; 96 T; 0 other;

Query Match 12.7%; Score 350; DB 21; Length 350;
 Best Local Similarity 100.0%; Pred. No. 3.3e-62;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 791 gagatagcctaatacgaacataatggaatttggaattccccaacacatacgaac 850
 DB 1 gagatagcctaatacgaacataatggaatttggaattccccaacacatacgaac 80
 QY 851 tttagagttgttggaagctgacgtgtaaacctgcgaagcttgctgaagaaatgaa 910
 DB 61 tttagagttgttggaagctgacgtgtaaacctgcgaagcttgctgaagaaatgaa 900
 QY 911 aatttgcacagatcgaaggaagatggtatggtgttttctctggtgacgtgtt 970
 DB 121 aatttgcacagatcgaaggaagatggtatggtgttttctctggtgacgtgtt 180
 QY 971 caaatgttacaagaagaagcctaataatctgttccagccttgccagatcccaag 1030
 DB 181 caaatgttacaagaagaagcctaataatctgttccagccttgccagatcccaag 240
 QY 1031 aagggtgataagagttacaagaagaagaagaagaagaagaagaagaagaagaaga 1090
 DB 241 aagggtgataagagttacaagaagaagaagaagaagaagaagaagaagaagaaga 300
 QY 1091 tatgatgatataccccaagatcatctctgtgtcatcccaaaccaagc 1140
 DB 301 tatgatgatataccccaagatcatctctgtgtcatcccaaaccaagc 350


```
RESULT 8
AAQ27370 ID AAQ27370 standard; cDNA; 2368 BP.
XX AC AAQ27370;
XX 27-JAN-1993 (first entry)
XX DE HUG-Br2.
XX Billirubin; UDP-glucuronosyltransferase; HUGBr1; HUGBr2;
XX monoglucuronide; diglucuronide; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 30..801
XX FT /*tag= a
XX FT polyA_signal 2347..2352
XX FT /*tag= b
XX FT /*number= 1
XX FT 2355..2360
XX FT /*tag= c
XX FT /number= 2
XX PM WO9212987-A.
XX PD 06-AUG-1992.
XX PF 10-JAN-1992; 92MO-US00282.
XX PR 10-JAN-1991; 91US-0639453.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX PI Owens IS, Ritter JK.
XX DR WPI: 1992-284593/34.
XX DR P-PSDB; AAR26154.
XX PT Isolated gene locus UGT1, DNA segments and diagnostic probes -
XX PT for diagnosing Gilbert's disease and Crigler-Najjar syndrome
XX PT types I and II
XX PS Disclosure: Fig 9A-I: 99pp; English.
XX CC Two human liver bilirubin UDP-glucuronosyltransferase cDNAs have
XX CC been isolated. They are referred to as HUGBr1 (AAQ27369) and HUGBr2
XX CC (AAQ27370) (Ritter, et al., J. Biol. Chem. 266:1043-1047 (1991)) and,
XX CC upon expression individually in COS-1 cells, encode isoforms that
XX CC catalyze the formation of the two bilirubin monoglucuronides and
XX CC the diglucuronide.
XX CC The cDNAs contain identical 3' ends (1469 bp in length) to each
XX CC other and to that of the human phenol transferase cDNA, HUGP1
XX CC (Harding et al., Proc. Natl. Aca. Sci. USA 85:8281 (1988)).
XX CC In contrast, they have unique 5' ends.
XX SQ Sequence 2368 BP; 609 A; 532 C; 566 G; 661 T; 0 other;

Query Match 11.5%; Score 317.8; DB 13; Length 2368;
Best Local Similarity 52.0%; Pred. No. 1.7e-55;
Matches 790; Conservative 0; Mismatches 717; Indels 12; Gaps 3;
```

```
QY 188 catgagtaacagiatgtgactcaatgaagccttggttaattgactacagaagcctct 247
   || ||| || || || || || || || || || || || || || || || || ||
Db 195 caacagcggtgtgtccaccaccaagaagtgatgacatcaagaagaattcttc 254
QY 248 gcatltaaatgtgagtgatgacatgacacagacagacaagaataatgaatatt 307
   || ||| || || || || || || || || || || || || || || || || ||
Db 255 accctgacagcctatgtctgttccatgaccag-----aaggaatttgatcggttaag 308
QY 308 gttagacctgactcgaatgtcttgcaggcttatacaactcggcaatcagttataaatta 367
   || ||| || || || || || || || || || || || || || || || || ||
Db 309 ctgggtacacccaagggtcttcttgaaacacacatctcttgaaagagatctcagaagt 368
QY 368 aatgatttttgttgaataagaggaactttaaataatgtgtgagagcttattacc 427
   || ||| || || || || || || || || || || || || || || || || ||
Db 369 atggcaattatgaacaatgacatgtacttgcacctcaatggtgtgtgagactgcat 428
QY 428 aatcagacgcttatgaagaagctacagagaaccaatacgaatgtatgttataagacct 487
   || ||| || || || || || || || || || || || || || || || || ||
Db 429 aatgagcgccctgatacagacactgaatgtactctcttgatgtgtttaaagagcccc 488
QY 488 gtgattcccttgtagaagcctgatagtgctgagtgctgacagtccttvtgtcacact 547
   || ||| || || || || || || || || || || || || || || || || ||
Db 489 gttaaccttcgcgggcggtgtgctgtaagtaacctgtcattcctcgttgtt---ttt 545
QY 548 agaatttcgtagagggaatatagtgagcgagctgtggaagaacttccagctccacttc 607
   || ||| || || || || || || || || || || || || || || || || ||
Db 546 tggaggtacatccatccatgtgacttaagagggacacagtgatccaaatccctctcc 605
QY 608 tatgtacctgtcctatgacagagactaacaagaatgaccttcttgaaagagtaaaa 667
   || ||| || || || || || || || || || || || || || || || || ||
Db 606 tatattccctaagttaactaacgacccaatltcagacacaatgacatctctgaaaggtcaag 665
QY 668 aattcaatgcttcaagtttgttccacttcgtgattcagaattacgatacctaatttgg 727
   || ||| || || || || || || || || || || || || || || || || ||
Db 666 aac---atgctacaccttcgtgcctgtccctgtctactacttgcatacttcttcccttat 722
QY 728 gaagagtttatagtaagcattaggaagccacatacttatgtagagcttgggaaaa 787
   || ||| || || || || || || || || || || || || || || || || ||
Db 723 gcaagctctgtcctctgagcttcttccagaagaggtgacgtgccagaacctattgagctct 782
QY 788 gctgagatactgctaaatacagacatacttggaatttggaaatttccctcaacatacaccct 847
   || ||| || || || || || || || || || || || || || || || || ||
Db 783 gactcgtctgctgtgttgaagtgacttggtaagatattacccttaggcacatcatgccc 842
QY 848 aacttgagttgttggaagatgtcacgtgtaacctgcacaagcttgcctaaggaatg 907
   || ||| || || || || || || || || || || || || || || || || ||
Db 843 aatatgtcttcatatgtggttcgtgacatcaactgttccacagggaaagccactactaggaatt 902
QY 908 gaaaatttgcacagaggttccagggaagatgtgtatgtgttctctcgtgggacactg 967
   || ||| || || || || || || || || || || || || || || || || ||
Db 903 gaagcctacatlaatgtcttcttgagaacatggaatgtgttctcttcttgaatcaatg 962
QY 968 ttcaaatgttacaagaagaagaagcctaataatcatgtcttccagccttgcaccatccca 1027
   || ||| || || || || || || || || || || || || || || || || ||
Db 963 gctcagaaatctccagagaagaagatgtgcaattgtcgtgacttgggcaaatccct 1022
QY 1028 cagaaggtttatgagtgatgacaaaggaaaaaaacatccacattagagccaatactgg 1087
   || ||| || || || || || || || || || || || || || || || || ||
Db 1023 cagacagctctgttggtgactgactggaaccgcacatgcaatcttgcgacaacacagata 1082
QY 1088 ctgtatgattgataccacagaatgtcttctgtgacacccaacaaacaaactttatc 1147
   || ||| || || || || || || || || || || || || || || || || ||
Db 1083 ctgtttaaagtgctacccaacaaagatcgtctgtgacacagtgacccggtcccttatc 1142
QY 1148 atcatatgtgagatgaatgtgacatcagaatatttaccatgggggtccctatgtgtgga 1207
   || ||| || || || || || || || || || || || || || || || || ||
Db 1143 acccatgtcgtgttcccatcagtggtttatgaagacatatgaaatgggttccatggtatg 1202
QY 1208 gtcccatatttgtgtatcagcttgataacatagctacatgaagaagcgaagcagct 1267
   || ||| || || || || || || || || || || || || || || || || ||
Db 1203 atgcccttgttggatcagatgagcaatgcaaatgcaatgagactaagagagactgta 1262
QY 1268 gtagaataaacttcaaaaactatgacaagcgaaagatttactagaggtctttagaacaagtc 1327
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Db      1263  gtgacctgagatgtctggaatgactctcgagatttagaanaatgtcctcaaaagcagtc 1322
Oy      1328  attaccgattccctcttaataagaaatgcatgattatcaagaattccacatgacaa 1387
Db      1323  atcaatgacaaaattacaagaacatcatcgctccctccagcttcaagaagaccgc 1382
Oy      1388  cctgtaagcccccatactgacagctctctgtagaggttttcacagccccaaga 1447
Db      1383  ccggtgagcgcctgagccctgcccgtctctgtagaggttttcacagccccaaga 1442
Oy      1448  gccaaagcctgagatcagctgcccacatgacctcctggttccagcactactatag 1507
Db      1443  gcgcacacaccctgcccgcagccacagacctcactcctgtagcagcactcctgac 1502
Oy      1508  gtattggtgtctctgctgactctgtggaacgtctatatctgttcacaaaatgttt 1567
Db      1503  gtgattggtctctctctgcccgtgctgtagcagtgccctcatcaacttaattgtt 1562
Oy      1568  ttatttctctgcaaaaat 1586
Db      1563  gcttatgctaccggaat 1581

```

RESULT 9

AAQ27369
ID AAQ27369 standard; cDNA; 2351 BP.

AC AAQ27369;

DT 27-JAN-1993 (first entry)

XX HUG-Brl.

KW Billirubin: UDP-glucuronosyltransferase; HUGBrl; HUGBr2;
KW monoglucuronide; diglucuronide; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 16..784

FT polyA_signal /tag= a

FT /tag= b

FT /number= 1

FT /tag= c

FT /number= 2

XX MO9212987-A.

PD 06-AUG-1992.

PE 10-JAN-1992; 92WO-US00282.

PR 10-JAN-1991; 91US-0639453.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

PI Owens IS, Ritter JK;

DR WPI; 1992-284593/34.

DR P-PSDB; AAR26153.

XX Isolated gene locus UGrl, DNA segments and diagnostic probes
PT for diagnosing Gilbert's disease and Crigler-Najjar syndrome
PT types I and II

PS Disclosure; Fig 9A-I; 99pp; English.

XX Two human liver billirubin UDP-glucuronosyltransferase cDNAs have
CC been isolated. They are referred to as HUGBrl (AAQ27369) and HUGBr2
CC (AAQ27370) (Ritter, et al., J. Biol. Chem. 266:1043-1047 (1991)) and,

CC upon expression individually in COS-1 cells, encode isoforms that
CC catalyse the formation of the two billirubin monoglucuronides and
CC the diglucuronide.
CC The cDNAs contain identical 3' ends (1466 bp in length) to each
CC other and to that of the human phenol transferase cDNA, HUGP1
CC (Harding et al., Proc. Natl. Aca. Sci. USA 85:8281 (1988)).
CC In contrast, they have unique 5' ends.

SQ Sequence 2351 BP; 602 A; 540 C; 556 G; 653 T; 0 other;

Query Match 11.5%; Score 316.6; DB 13; Length 2351;

Best Local Similarity 52.3%; Pred. No. 3e-55;

Matches 775; Conservative 0; Mismatches 694; Indels 12; Gaps 3;

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Oy      106  tgggaagtcctgtgtgcccctgacatgagcactgtgcttaagtcaagtcattct 165
Db      96  tgggaagatctgttgcctccagtgatgagcactgtgagcatgcttgaggccat 155
Oy      166  agaaagctcatagtagaagggccatgaggtaacagattgactactcaaacgttcgt 225
Db      156  ccagcagctgcagcagagggaacatgaatagtgtcctlagcacctgaagccctgtgta 215
Oy      226  aattgactacaggaagccctctgcatgaaatttgagtggtgtccatgccaagacag 285
Db      216  catcagaagacggagcatttacaacctga-----agacgtacccgtgcatccaag 269
Oy      286  aacagaagaanaatgaaatatgttgcacctagctcgtgaatgtcttgcaggcttaaac 345
Db      270  ggaagatgtagaaagctcttctgttagctcgcgacataatgttttgagaatgatctt 329
Oy      346  ctggcaatcagttataaataatgattttttgttgtaataaagaggaacttaaat 405
Db      330  cctgacgctgtgatacaacaacatacaagaanaaagaagactctgtcatgtcttctgc 389
Oy      406  gatgtgtagagcttatcatcaatcagacgtctatgaaagactgacaaacaacta 465
Db      390  tgcgtgtcccaacttactacacaagaagactatgctcctccgcgcaagaagacgtc 449
Oy      466  cgattgaagctatagaccctgtgattctcctgtgagacccgtgagctgtgattctgc 525
Db      450  tgatgtcagctggaagagccctctctctgcagcccaactggtgcccagctactctc 509
Oy      526  agtcccttctgtcctcaacttagaattctgtgaggaagcaatagaggcggaagctg 585
Db      510  tctgcccaactgattc-----tcttgatgacactgcaagcagcctggaatttgagctac 566
Oy      586  gaaactccagctccacttccatgtatcctgtgacactgacatgacaggaactaagaga 645
Db      567  ccagtgccccaaccacatctctctacgtgtccagagcctctctctctcatcagatcacat 626
Oy      646  gaccttctggaagagtaaaaaatcaatgtcttcagtttgttctccctctgattca 705
Db      627  gaccttctgcaagcggtgaaagaa---catgtcatgtccttcaagaacttctgtg 683
Oy      706  ggattaagactatacttcttggaagagtttatagtaaggcataggaagggccaactac 765
Db      684  cgaagtgttattatcccccgtatgcaacctgtgccacagaattccttcagagagaggtac 743
Oy      766  attatgtagagctgtgggaaagcgtgagatagtgttaataagacatatgtggatttga 825
Db      744  tgtccaggaactattgaactgtcgtcatcgtctgtgtttagaagtgacttgtgaaga 803
Oy      826  attcctcaacataccaactaactttagattgttgttgaagattgcctgtaaacctgc 885
Db      804  ttacctagagcccatcagtgccaataatgttggttgttggaatcaactgcttcaaca 863
Oy      886  caaagcttgcctaaagaaatgaaatattgtccagaagttcagggaagaatgtatgt 945
Db      864  aaatccatcaccaggaattgaaagcattaaatgactctggaagaacatgaaatgt 923
Oy      946  ggtttctctctggggcagcttcaaaatggtacagaagaagaagctatatactatgc 1005

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```
DB 924 gtttctcttggatcaatggtctcagaattccagagaagaagctatgacattgc 983
QY 1006 ttcagcccttgccagatcccaagaagtggtatagaggtacaagaagaaaaacatc 1065
DB 984 tgaagcttggcacaataccctccagacagctctggtggtacactggaacccgacatc 1043
QY 1066 cacattggagcccaatcctgcgtgtatgtttgatacccccagatatctctgttca 1125
DB 1044 gaatcttgcaacaacaacagatactgtttaagttggtaccaccaaacgactctgtgtca 1103
QY 1126 tcccaaaccaaaagcttttaccctcagctggtggaatgagatggagatcctagaattta 1185
DB 1104 ccgagtggaccggtgaccttatccaccatgctgttcccatggtgtttatgaagacatatg 1163
QY 1186 ccattggttccctatggttggaggttcccaattttgtgtatcagcttataacatagctca 1245
DB 1164 caatggtcttcccatggttgaatgaccccttgttggatcagaatggacaatgcaaacgcg 1223
QY 1246 catgaagcccaaaaggaacagctgtagaataaacttcaaaactatggcaagcgagaattt 1305
DB 1224 catggaactcaaaaggaagctgtgagaccctgtgaatgtcttggaaatgacttctgaagatt 1283
QY 1306 actgagggcttggagaacagctatcaccgattccctctataaagaagatgctatgagatt 1365
DB 1284 agaaaatgctcaaaaagcagctatcacaatgacaagaagtacaagagaacatcatgctgct 1343
QY 1366 atcaagaatccacaatgataacctgttaagccccctagatcgagcagcttctgtgacga 1425
DB 1344 ctccagcttccacaagaagccgcggtgagccgctgagaccgtgctgtctgtgtgtgga 1403
QY 1426 gtttgtatgcgcaaaaagagcaagcaagcccttgcagtcagctccatgagccctcacctg 1485
DB 1404 gttgtgtatgaggaacaagggcgcgccacaccttgcgcgcgcagcccaagcctcaccctg 1463
QY 1486 gtcccaagcactactctataatggtatggttgccttgcctgacccgtgtggcaactgctat 1545
DB 1464 gtaccagctaccatctccttgcagctgattgttctccttgcgtgcgtgcgaagcggc 1523
QY 1546 attcctgttcaaaaatggtttttatttcttctcctgtcaaaaat 1586
DB 1524 ctcaatcactttaaatgttgtgttattgtgtctaccggaat 1564

RESULT 10
AAZ45118
ID AAZ45118 standard; DNA: 735 BP.
XX
AC AAZ45118;
XX
DT 28-FEB-2000 (first entry)
XX
DE UDP-glucuronosyltransferase 1 (UGT1) exons 2-5 nucleotide sequence.
XX
KW uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe;
KW glucuronic acid; Crigler-Najjar syndrome; Gilbert syndrome; jaundice;
KW unconjugated hyperbilirubinemia; drug metabolism; transgenic animal;
KW pharmacogenetic screening; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN MO9957322-A2.
XX
PD 11-NOV-1999.
XX
PF 04-MAY-1999; 99MO-US09702.
XX
PR 07-MAY-1998; 98US-0084807.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Penny L, Galvin M;
XX
DR WPI, 2000-052981/04.
```

```
DR P-PSDB; AAY57100.
XX
XX New nucleic acid representing polymorphisms in the human uridine
PT diphosphate glucuronosyltransferase gene, used for diagnosis and
PT evaluation of drug metabolism
XX
XX Examples: Page 43-44; 63pp; English.
PS
XX
XX Nucleotide sequences AAZ45110-245118 are exons 1A-1J of the human
CC uridine diphosphate-glucuronosyltransferase 1 (UGT1) gene. The UGTs are a
CC family of enzymes that catalyze the glucuronic acid conjugation of a wide
CC range of endogenous and exogenous substrates including phenols,
CC alcohols, amines and fatty acids. Many of the reactions catalysed by UGTs
CC result in toxic substances being converted to compounds which are more
CC water soluble and are excreted. The invention relates to and identifies
CC UGT1 polymorphisms (AAZ45004-245041). The polymorphism sequences are
CC useful as probes for detecting UGT1 locus polymorphisms, indicative of
CC altered UGT1 expression or activity. These polymorphisms are associated
CC with Crigler-Najjar and Gilbert syndromes (unconjugated
CC hyperbilirubinemia) and drug metabolism. The genotyping of the UGT1 gene
CC is used to predict the rate of metabolism of UGT1 substrates, possible
CC drug-drug interactions and adverse side effects (i.e. to optimize drug
CC dosage), and to screen for diseases caused by exposure to toxins and to
CC study the effects of polymorphisms on enzymatic activity. The UGT1
CC sequences, including polymorphisms, can also be used to produce the
CC corresponding protein (or its fragments) or to generate transgenic
CC animals or modified cells e.g. for pharmacogenetic screening.
XX
XX
SQ Sequence 735 BP; 189 A; 179 C; 187 G; 180 T; 0 other;

Query Match 9.9%; Score 272.2; DB 21; Length 735;
Best Local Similarity 62.38; Pred. No. 2.3e-46;
Matches 427; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

QY 902 gaatggaaaatttcttccagagttcaggggaagatggtatgtgttctctcgtgg 961
DB 1 gaattgaagctcatcaatgaatgcttctggaagaacatggaattggtttctcttggga 60
QY 962 tcaatgttccaanaatgtctacagaagaagaagctaatatcatgttctcagcccttgccag 1021
DB 61 tcaatgttctcagaatctccagagaagaagctatgtaactgtatgtatgttggcaca 120
QY 1022 atcccaagaagtggttatagaggtacaaaggaaaaaaacatccatttggagccat 1081
DB 121 atccctcagacagctcgttggcggtacacttgaacccgacatcgaatcttgcgaacac 180
QY 1082 actgcgtgtatgttggatgcccaagaatgattcttctgttcatcccaaaacaaagct 1141
DB 181 acgataactgtttaaagtgctaccccaaaacgactgctgtgtccacgaatgacccgtgcc 240
QY 1142 ttatacactcagtggtgaatgaatggtatcagatcagatattaccatgggttccatg 1201
DB 241 ttatacaccatgtctgttcccatggtgtttatgaagaacatgcaatgagtggttccatg 300
QY 1202 gtggaggttcccatatttgttgcacgttgaatacatagctacatagaagggccaagga 1261
DB 301 gtgatgtgaccttgttgtgtgacagatgacaatgacaagcgatgagacataagga 360
QY 1262 gcaactgtagaataaacttcaaaactatgcaagcgagaagtcttactgaagggtttgga 1321
DB 361 gctgagtgaccctggaatgtcttgaatgactcttcgaagatttgaanaatgacctaa 420
QY 1322 acaatcattaccagattccctctataaagaagatgctatgatatatacaagaattcacat 1381
DB 421 gcaatcacaatgacaagaagttacaagaagacatcatgcccctccagccttcaagaag 480
QY 1382 gataacctgtaagccctcagatcgagcagcttcttggatcgagttgttcatgctgacac 1441
DB 481 gaccgcccgtgtagcgcgtgacactgtgcgttctgtgtgtgagttgtgtatgagcacc 540
QY 1442 aaaggaagcaagcaccctgagctcagctgcccatacctcacttggttccacacatctct 1501
```

Query Match	7.3%;	Score 200.2;	DB 21;	Length 2312;
Best Local Similarity	56.6%;	Pred. No. 1.2e-31;		
Matches 417; Conservative	0;	Mismatches 308;	Indels 12;	Gaps 2

XX
2
1
1
1
1
1
1

PN WC20010/665-A2.
XX
XX
PD 01-FEB-2001.
XX

```
PF 26-JUL-2000; 2000MO-US20476.
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
CC
SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match      7.1%; Score 196.4; DB 22; Length 936;
Best Local Similarity 0.6%; Pred. No. 5.6e-31;
Matches 5; Conservative 548; Mismatches 229; Indels 0; Gaps 0;

QY 1773 tatactcattcttgctgatttccctagtggtgcttactcctctctcacttgtg 1832
DB 4 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 63
QY 1833 acacaggacatgatacatcctaatttctctatcttgatatacactglttcagcgt 1892
DB 64 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 123
QY 1893 cattactctctaacttaagtgatagggtagcctgcaatagctgattcctggtgtg 1952
DB 124 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 183
QY 1953 cacaacacatgtagtgaagaatgaataatgtaaaattcacaaattcagtaaacac 2012
DB 184 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 243
QY 2013 acaaatcaatgaagcattctatgacattagctgtgtatgagtaacataatgttttct 2072
DB 244 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 303
QY 2073 tttaaatltaataagcccttctacataccagcattacgtatctcagacaatgattgc 2132
DB 304 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 363
QY 2133 taaaatagcagatagggcattacactcagaatagtttgctatttccatactactc 2192
DB 364 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 423
QY 2193 tagatgcatagcctacattctgcatcacttaactgacatttttggttgcttgat 2252
DB 424 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 483
QY 2253 gataaatagacgttcttatattgtcctcaataataaagaactgaaatttcttac 2312
DB 484 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 543
QY 2313 atagagaaaagtccataagatattcaagttaaacagatttttgagataagtaaacat 2372
DB 544 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 603
QY 2373 tagaataatgattgttaatttctgatttataaatttaattgattgatacttgatt 2432
DB 544 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 603
```

```
DB 604 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 663
QY 2433 taatgtctcttcttaaatgtagatactcataattctctctctatatacaaaagta 2492
DB 664 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 723
QY 2493 taattactgtagaaaataaagatgctgttctgaaagtaaaaaaaaaaaaaaa 2552
DB 724 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 783
QY 2553 aa 2554
DB 784 ww 785

RESULT 13
AAF58254
ID AAF58254 standard; DNA; 936 BP.
XX
XX AAF58254;
AC
XX
XX 24-APR-2001 (first entry)
DT
XX
XX Oligonucleotide D1875.
DE
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
KM
XX
XX gene expression; ss.
KM
XX
XX Synthetic.
OS
XX
XX WO200107665-A2.
PN
XX
XX 01-FEB-2001.
PD
XX
XX 26-JUL-2000; 2000MO-US20476.
PF
XX
XX 26-JUL-1999; 99US-0145695.
PR
XX
XX 17-MAR-2000; 2000US-0190259.
PR
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
PA
XX
XX Umek RM;
PI
XX
XX WPI; 2001-159728/16.
DR
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
CC
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match      7.1%; Score 196.4; DB 22; Length 936;
Best Local Similarity 0.6%; Pred. No. 5.6e-31;
Matches 5; Conservative 548; Mismatches 229; Indels 0; Gaps 0;

QY 1773 tatactcattcttgctgatttccctagtggtgcttactcctctcacttgtg 1832
DB 4 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 63
QY 1833 acacaggacatgatacatcctaatttctctatcttgatatacactglttcagcgt 1892
DB 64 www.wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 123
```

```

QY 1893 cattactctctaaccttaagtatgtagggtgacgtgcaatatgctactctgtgttg 1952
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 183
QY 1953 cacaaacacatgcatgtaagaagtaaaaaatgtaaaatcacaataatcagtaaaccc 2012
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 243
QY 2013 acaaatcaatgaagcaatctgacatctagctgttatgtatgtagtaaatgattttctt 2072
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 303
QY 2073 ttccaatttaaatgaagccctctacataccagcaatctgactgctcagaatgattgc 2132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 363
QY 2133 taaaatgacgaaggcattacaccagaatagttgtctatatctccacatacctcacc 2192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 423
QY 2193 tagatgcatagcattcctgcatcactgaactgaactttttgtgtgttgat 2252
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 483
QY 2253 gataaatagacagtcctctatttctcctcacaataaagaagaactgaatttctctac 2312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 543
QY 2313 atagagaagaatgcatagaatattcaagttaaacgattattttgagataagtaacct 2372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 544 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 603
QY 2373 tagaataatgattgtaattctctgatttataaaatttaattgtagtacactgatt 2432
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 604 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 663
QY 2433 taaatgctatcctttaaaatgatgatactcactaattcctatctcataatcaaaagta 2492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 664 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 723
QY 2493 taattactgtagaagaataaagagatgcttctgtctgaaagtataaaaaaa 2552
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 724 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 783
QY 2553 aa 2554
   : :
Db 784 ww 785

```

RESULT 14

```

AAF58257
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
   gene expression; ss.
XX
OS Synthetic.
XX
PN MO200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX

```

```

PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
XX WPI; 2001-159728/16.
XX
DR
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

```

Query Match 7.1%; Score 196.4; DB 22; Length 936;
 Best Local Similarity 0.6%; Pred. No. 5,6e-31;
 Matches 5; Conservative 548; Mismatches 229; Indels 0; Gaps 0;

```

QY 1773 tatatctctctctgctgctcatttcctcagtggtctactctctcctaactgtg 1832
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 63
QY 1833 acacaaggaatgataacataaatttcctatttctgatacactgttccatgact 1892
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 123
QY 1893 cattactctctaaccttaagtatgtagggtgacgtgcaatatgctactctgtgttg 1952
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 183
QY 1953 cacaaacacatgcatgtaagaagtaaaaaatgtaaaatcacaataatcagtaaaccc 2012
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 243
QY 2013 acaaatcaatgaagcaatctgacatctagctgttatgtatgtagtaaatgattttctt 2072
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 303
QY 2073 ttccaatttaaatgaagccctctacataccagcaatctgactgctcagaatgattgc 2132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 363
QY 2133 taaaatgacgaaggcattacaccagaatagttgtctatatctccacatacctcacc 2192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 423
QY 2193 tagatgcatagcattcctgcatcactgaactgaactttttgtgtgttgat 2252
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 483
QY 2253 gataaatagacagtcctctatttctcctcacaataaagaagaactgaatttctctac 2312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 543
QY 2313 atagagaagaatgcatagaatattcaagttaaacgattattttgagataagtaacct 2372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 544 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 603
QY 2373 tagaataatgattgtaattctctgatttataaaatttaattgtagtacactgatt 2432
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 604 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 663
QY 2433 taaatgctatcctttaaaatgatgatactcactaattcctatctcataatcaaaagta 2492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 664 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 723

```

[illegible]

RESULT 15

AAAF58259

ID AAF58259 standard; DNA; 936 BP.

AC AAF58259;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D2004

KM Electron-transfer group; ETM; mismatch; genotyping;

KW gene expression; ss.

OS Synthetic.

PN W0200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US20476.

PR 26-JUL-1999; 99US-0145695.

XX

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI Umek RM;

DR WPI; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in PT hybridization assays, e.g. for genotyping, allowing repeat analyses on PT a single surface -

PS Example 6; Page 128; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.

Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match	7.18;	Score 196.4;	DB 22;	Length 936;

Best Local Similarity 0.68; Pred. No. 5.6e-31;

Matches 5; Conservative 548; Mismatches 229; Indels 0; Gaps 0;

QY 1773 tatactcattcttgcgtgcatttctcctagtggtgcttactctctctcaacttgtg 1832

[illegible]

1833 acacaaggaatgatacatctaaatttccctatttctgataatcactgtttccatgacgc 1839

Dd 64 WWWWWWWWWWWWWWWW C WWWWWWWWWWWWWWWWW L 23

[illegible]

Search completed: August 13, 2001, 12:27:18
Job time: 6449 sec

